AMENDMENT TO THE SPECIFICATION

Please replace paragraph on page 2, line 8 with the following amended paragraph:

This invention was made with government support under Grant number 5P01H601323-03 from the National Institute[[s]] of Health. Accordingly, the U.S. Government retains certain rights in the invention.

Please replace paragraph on page 13, line 15 with the following:

"Nucleic acids," according to the present invention, may include any polymer or oligomer of nucleosides or nucleotides, which include pyrimidine and purine bases, preferably cytosine, thymine, and uracil, and adenine and guanine, respectively. See Albert L. Lehninger, PRINCIPLES OF BIOCHEMISTRY, at 793-800 (Worth Pub. 1982). Indeed, the present invention contemplates any deoxyribonucleotide, ribonucleotide or peptide nucleic acid component, and any chemical variants thereof, such as methylated, hydroxymethylated or glucosylated forms of these bases, and the like. The polymers or oligomers may be heterogeneous or homogeneous in composition, and may be isolated from naturally-occurring sources or may be artificially or synthetically produced. See U.S. patent application Serial No. 08/630,427, now U.S. Pat. 6,156,501, issued on December 5, 2000, which is incorporated herein by reference in its entirety for all purposes. In addition, the nucleic acids may be DNA or RNA, or a mixture thereof, and may exist permanently or transitionally in single-stranded or double-stranded form, including homoduplex, heteroduplex, and hybrid states. Oligonucleotide

and polynucleotide are included in this definition and relate to two or more nucleic acids in a polynucleotide.

Please replace paragraph on page 15, line 3 with the following:

An "array" may comprise a solid support with peptide or nucleic acid probes attached to said support. Arrays typically comprise a plurality of different nucleic acid or peptide probes that are coupled to a surface of a substrate in different, known locations. These arrays, also described as "microarrays" or colloquially "chips" have been generally described in the art, for example, U.S. Pat. Nos. 5,143,854, 5,445,934, 5,744,305, 5,677,195, 6,040,193, 5,424,186 and Fodor et al., Science, 251:767-777 (1991). Each of which is incorporated by reference in its entirety for all purposes. These arrays may generally be produced using mechanical synthesis methods or light directed synthesis methods which incorporate a combination of photolithographic methods and solid phase synthesis methods. Techniques for the synthesis of these arrays using mechanical synthesis methods are described in, e.g., U.S. Pat. Nos. 5,384,261, and 6,040,193, which are incorporated herein by reference in their entirety for all purposes. Although a planar array surface is preferred, the array may be fabricated on a surface of virtually any shape or even a multiplicity of surfaces. Arrays may be peptides or nucleic acids on beads, gels, polymeric surfaces, fibers such as fiber optics, glass or any other appropriate substrate, see U.S. Patent Nos. 5,770,358, 5,789,162, 5,708,153, 6,040,193 and 5,800,992, which are hereby incorporated in their entirety for all purposes. Arrays may be packaged in such a manner as to allow for diagnostics or other manipulation of in an all inclusive

device, see for example, US Patent Nos. 5,856,174 and 5,922,591, and 5,945,334, which are incorporated herein in their entirety by reference for all purposes. See also U.S. patent application Serial No. 09/545,207 currently pending which is incorporated herein in its entirety for all purposes for additional information concerning arrays, their manufacture, and their characteristics. It is hereby incorporated by reference in its entirety for all purposes.

Please replace paragraph on page 30, line 9 with the following:

Germline mutations in BRCA1 are present in 50-60% of kindreds with breast and ovarian cancer, and may account for approximately 2-5% of all breast cancer cases in the general population (Hall et al., *Science* 250, 1684-1689 (1990), Narod et al., *Lancet* 338, 82-83 (1991), Easton et al. *Am. J. Hum. Genet.* 52, 678-701 (1993), Rowell et al., *Am. J. Hum. Genet.* 55, 861-865 (1994)). Heterozygous carriers are markedly predisposed to early onset breast and ovarian cancer, and are also at moderately increased risk of developing colon and prostate cancer (Ford et al., *Lancet* 343, 692-695 (1994)). The protein coding region of BRCA1 contains 5,592-bp in 22 coding exons spread over 100-kb of genomic DNA (Miki et al., *Science* 266, 66-71 (1994)). Over 111 unique BRCA1 mutations distributed throughout the gene have been described in the literature (Shattuck-Eidens et al., *Am. Med. Assoc.* 273, 535-541 (1995) and (Breast Cancer Information Core Database located on the *World Wide Web* ~~*at http://www.nchgr.nih.gov/Intramural-research/Lab-transfer/Bic/.*~~)). Most of these are frameshift, nonsense, or splice mutations resulting in a disruption of the normal reading frame. Except for the Ashkenazi Jewish population, where two mutations account for the majority of BRCA1 alterations

(Struewing et al., *Am J. Hum. Genet.* 57, 1-7 (1995); Struewing et al., *Nature Genet. 11,* 198-200 (1995); Tonin et al., *Am. J. Hum. Genet.* 57, 189 (1995); Friedman et al., *Am. J. Hum. Genet.* 57, 1284-1297 (1995); FitzGerald et al., *N. Engl. J. Med.* 334, 143-149 (1996); Offit et al., *Lancet* 347, 1643-1645 (1996)), allelic heterogeneity confounds the ability to identify BRCA1 mutation carriers by methods (such as allele-specific oligonucleotide [ASO] hybridization) which detect only a finite set of previously described mutations.

Please replace paragraph on page 31, line 11 with the following:

PCR reactions were performed on genomic samples using the EXPAND™ Long Range PCR Kit (Boehringer Mannheim) with primers 11FT3 (SEQ ID NO: 01) 5'-ATTAACCCTCACTAAAGGGAATTAAATGAAAGAGTATGAGC-3' and 11RT7 (SEQ ID NO: 02) 5'-TAATACGACTCACTATAGGGAGTGCTCCCAAAAGCATAAA-3' containing T3 and T7 RNA polymerase promoter sequences respectively. In vitro transcription reactions from these exon 11 amplicon templates were performed in 10 μl reaction volumes using T3 RNA polymerase transcription buffer (Promega), 0.7 MM of ATP, CTP, GTP, and UTP, 10 MM DTT, 0.7 MM fluorescein-12-UTP or 0.15 MM biotin-16-UTP (Boehringer Mannheim) for reference and test samples respectively, and 1OU T3 or T7 RNA polymerase as indicated.

Please replace paragraph on page 32, line 1 with the following:

A reference template was generated from PCR amplification of exon 11 from a *BRCA1* cDNA clone. Reference and test sample transcription products were diluted to a final concentration of 100 nM in a 25 µl solution of 30 mm $MgCl_2$. The reaction was incubated at 94°C for 70 minutes to fragment targets (Lipshutz, et al., *BioTechniques* 19, 442-447 (1995); Kozal, et al., *Nature Med.* 2, 753-759 (1996)). Cofragmented targets were diluted 1/100 into a 300 pl volume of hybridization buffer (3 M TMAC-Cl (tetramethylammonium chloride), 1x TE pH 7.4, 0.001% Triton X-100, 1 nM 5'-fluorescein-labelled control oligonucleotide (SEQ ID NO: 03) 5'-CGGTAGCATCTTGAC-3'). This control oligonucleotide is designed to hybridize to specific surface probes to aid in image alignment. Target was hybridized with the chip in a 250 µl volume for 4 hours at 35°C. The chip surface was washed with 10 ml of wash buffer (6X SSPE, 0.001% Triton X-100) and stained with phycoerythrin-streptavidin conjugate (Molecular Probes) (2 µg/ml in wash buffer) for 5 minutes at room temperature. The chip was washed with 10 ml of wash buffer and scanned as described (Lipshutz et al., *BioTechniques* 19, 442-447 (1995); Kozal et al., *Nature Med.* 2, 753-759 (1996)). Hybridization signals were detected by a photomultiplier tube using 515-545 nm bandpass and 560 nm longpass emission filters for fluorescein reference (green) and biotin test (red) samples respectively (Cronin et al., *Hum. Mut.* 7, 244-255 (1996); Chee et al., Science 274, 610-614 (1996)).

Please replace paragraph on page 32, line 20 with the following:

Four pairs of PCR primers (P1M13+ (SEQ ID NO: 04) 5'-GTTTCCCAGTCACACGGAATTAAATGAAAG AGTATGAGC-3' and PIM13- (SEQ ID NO: 05) 5'-AGGAAACAGCTATGACCATGTGAGGGGACGCTCT TG-3', P2M13+ (SEQ ID NO: 06) 5'-GTTTCCCAGTCACACGTTGGGAAAACCTATCGGAA-3' and P2M13 (SEQ ID NO: 07) 5'-AGGAAACAGCTATGACCATCTTTGGGGTCTTCAGCA-3', P3M13+ (SEQ ID NO: 08) 5'-GTTTCCCAGTCACACGTGTTCAAATACCAGTGAACTTA-3' and P3M13- (SEQ ID NO: 09) 5'-AGGAAACAGCTATG ACCATGGAGCCCACTTATTAGTAC-3', P4M13+ (SEQ ID NO: 10) 5'-GTTTCCCAGTCACACGCCAAGT ACAGTGAGCACAATTA-3' and P4M13- (SEQ ID NO: 11) 5'-AGGAAACAGCTATGACCATGTGCTCCC AAAAGCATAAA-3') were designed to generate four partially overlapping amplicons which cover the entire sequence of exon 11 and contain M13 forward and reverse sequences at the 5'-end of either strand Depending on region to be analyzed one of the four amplicons was generated from the appropriate genomic sample using the EXPAND™ Long Range PCR kit (Boehringer Mannheim) with the recommended protocol. Dye primer dideoxysequenciong reactions were performed using AmpliTaq DNA Polymerase FS kit (Perkin Elmer) with the suggested protocol and either M13 forward or M13 reverse DYEnamic™ energy transfer dye primers (Amersham Life Science).